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By [Signature]

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

17169/04

In re the Application of)	
Thompson, G., et al.)	Serial No. 07/762,762
Examiner: Leguyader, J.)	Allowed: August 2, 1999
Filed: September 16, 1991)	Batch No.: W48
For: <u>PLANT DESATURASES</u>)	SUBMISSION OF SUBSTITUTE
<u>COMPOSITIONS AND USES</u>)	DRAWINGS UNDER 37 CFR
)	1.84

Honorable Commissioner of
Patents and Trademarks
Washington, DC 20231

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OFFICIAL DRAFTSMAN

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Dear Sir:

This letter is in response to the Draftsmen's comments mailed on August 2, 1999 objecting to the drawings as submitted by Applicants in a communication of September 16, 1991. Provided herewith are substitute drawings for Figure 1-10. The substitute drawings are in compliance with the requirements for formal drawings made in this case under 37 CFR § 1.84.

No substantial modifications have been made to these substitute drawings.

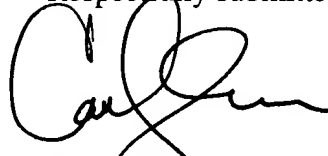
A conditional petition for an Extension of Time is requested to provide for the timely filing if an extension of time is required after all papers filed with this transmittal have been considered.



The Commissioner is GENERALLY authorized to charge any required fees, with the exception of an Issue Fee, relating to this paper to Deposit Account No. 03-0173.

In the event that there are any questions regarding these Figures, the Draftsman is invited to contact the undersigned at (530) 753-6313.

Respectfully submitted,



Carl J. Schwedler
Reg. No. 36,924

CALGENE LLC
1920 Fifth Street
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Enclosure: Figures 1-10

ASTLGSTPKVDNAKKPFQPPREVHVQVTH^S MPPQKIEIFKSI^WEG^R AEQNILV^H_F LKPVEKWCWQ

F2: DFLPDP^SA_T EGFDEQVKELRARAKEIPDDYFVVLVGDMITEEALPTYOTMLNTLDGV

F3: DETGASLTPWAVWT

F4: DLLHTYLYLSGRV

F5: DMRQIQKTIQYLI

F6: TENSPLYLGFYTSFQER

F7: DV^K_F LAQI^C_Q GTIASDEKRRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI^S_T MPAHLMY

F8: DNLF

F9: dvFLAV^A_I QRL^G_I VYTAK

F10: DYADILEFLVGRWK

F11: VADLTGLSGEGRKAQ^Q_G DYVCGLPPRI^RRRLEERAQGRAKEGPVVPFSWIFDRQVKL

FIGURE 1

HindIII
 1 GCTCACTTGTGTGTGGAGAGAAAAACAGAACTCACA AAAAGCTTTGCGACTGCCAAGAACACAACA
 69 42

70 ACAACAAGATCAAGAAGAAGAAGATCAAAAATGGCTCTTTCGAATCACTCCAGTGACCTTGCAA
 138 METAlaLeuArgIleThrProValThrLeuGln

EcoRV BglII NcoI
 139 TCGGAGAGATATCGTTCGTTTTCGTTTCCCTAAGAAGGCTAATCTCAGATCTCCCAAATTCGCCCATGGCC
 207 SerGluArgTyrArgSerPheSerPheProLysLysAlaAsnLeuArgSerProLysPheAlaMETAla
 149 185 201

HindII
 208 TCCACCCCTCGGATCATCCACACCGAAGGTTGACAAATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTT
 276 SerThrLeuGlySerSerThrProLysValAspAsnAlaLysLysProPheGlnProProArgGluVal
 238

277 CATGTTCAGGTGACGCACTCCATGCCACCACAGAAGATAGAGATTTTCAAATCCATCGAGGGTTGGGCT
 345 HisValGlnValThrHisSerMETProProGlnLysIleGluIlePheLysSerIleGluGlyTrpAla

346 GAGCAGAACATATTGGTTACCTAAAGCCAGTGGAGAAAATGTTGGCAAGCACAGGATTTCTTGCCCGGAC
414

GluGlnAsnIleLeuValHisLeuLysProValGluLysCysTrpGlnAlaGlnAspPheLeuProAsp

415 CCTGCATCTGAAGGATTTGATGAACAAGTCAAGGAACCTAAGGGCAAGAGCAAAAGGAGATTCCTGATGAT
483
ProAlaSerGluGlyPheAspGluGlnValLysGluLeuArgAlaAlaLysGluIleProAspAsp
484 TACTTTGTTGTTTTGGTTGGAGATATGATTACAGAGGAAGCCCTACCTACTTACCAAACAATGCTTAAT
552
TyrPheValValLeuValGlyAspMETIleThrGluGluAlaLeuProThrTyrGlnThrMETLeuAsn
553 ACCCTAGATGGTGTAACGTGATGAGACTGGGGCTAGCCCTTACGCCCTTGGGCTGTCTGGACTAGGGCTTGG
621
ThrLeuAspGlyValArgAspGluThrGlyAlaSerLeuThrProTrpAlaValTrpThrArgAlaTrp
PvuII
|
622 ACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACCTATCTACCTTTCTGGCGGGTAGACATG
690
ThrAlaGluGluAsnArgHisGlyAspLeuLeuHisThrTyrLeuTyrLeuSerGlyArgValAspMET
684
BamHI
|
691 AGGCAGATACAGAAGACAATTTCAGTATCTCATTTGGGTCAGGAATGGATCCCTCGTACCAGAAACAGCCCC
759
ArgGlnIleGlnLysThrIleGlnTyrLeuIleGlySerGlyMETAspProArgThrGluAsnSerPro
736

FIGURE 2
Page 3 of 7

760 TACCTTGGGTTTCATCTACACATCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAACACCGCCAGG
828 TyrLeuGlyPheIleTyrThrSerPheGlnGluArgAlaThrPheValSerHisGlyAsnThrAlaArg

SphI
 |
 829 CATGCAAAGGATCATGGGACGTGAAACTGGCGCAAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGT
 897
 HisAlaLysAspHisGlyAspValLysLeuAlaGlnIleCysGlyThrIleAlaSerAspGluLysArg
 833

 ClaI
 |
 898 CACGAGACCGCTTATACAAAGATAGTCGAAAAGCTATTCGAGATCGATCCTGATGGCACCGTTCCTTGCT
 966
 HisGluThrAlaTyrThrLysIleValGluLysLeuPheGluIleAspProAspGlyThrValLeuAla
 942

 BglII
 |
 967 TTTGCCGACATGATGAGGAAAAAGATCTCGATGCCCGCACACTTGATGTACGATGGGCGTGATGACAAC
 1035
 PheAlaAspMETMETArgLysLysIleSerMETProAlaHisLeuMETTyrAspGlyArgAspAsn
 990

 AccI
 |
 1036 CTCTTCGAACATTTCTCGGCGGTGCCCCAAAGACTCGGCGTCTACACCGCCAAAGACTACGCCGACATA
 1104
 LeuPheGluHisPheSerAlaValAlaGlnArgLeuGlyValTyrThrAlaLysAspTyrAlaAspIle
 1077

1105 CTGGAATTCTGTCTGGGCGGTGGAAAGTGGCGGATTTGACCGGCCCTATCTGGTGAAGGCGGTAAAGCG
1173
LeuGluPheLeuValGlyArgTrpLysValAlaAspLeuThrGlyLeuSerGlyGluGlyArgLysAla

1174 CAAGATTATGTTTGC GG GTTGC CACCAAGAAATCAGAAAGGCTGGAGGAGAGAGCTCAAGGGCGAGCAAAG
1242 GlnAspTyrValCysGlyLeuProProArgIleArgArgLeuGluGluArgAlaGlnGlyArgAlaLys
1228

SacI

1243 GAAGGACCTGTTGTTCCATTTCAGCTGGATTTCGATAGACAGGTGAAGCTGTGAAGAAAAAACA
1311 GluGlyProValValProPheSerTrpIlePheAspArgGlnValLysLeu
1266

PvuII

1312 GCAGTGAGTTCGGTTTCTGTGGCTTATTGGGTAGAGGTTAAAAACCTATTTTAGATGTCTGTTTCGTGT
1380

1381 AATGTGGTTTTTTTTCTTAATCTGAATCTGGTATTGTGTCGTTGAGTTCGCGTGTGTGTAACCTTG
1449

1450 TGTGGCTGTGGACATAATTATAGAACTCGTTATGCCAATTTTGATGACGGTGGTTATCGTCTCCCCCTGGT
1518

1519 GTTTTTTTTATTGTTT 1533

AAAAGAAAAA GGTAAGAAAA AAAACA	ATG GCT CTC AAG CTC AAT CCT TTC CTT TCT	56
	MET Ala Leu Lys Leu Asn Pro Phe Leu Ser	
CAA ACC CAA AAG TTA CCT TCT TTC GCT CTT CCA CCA ATG GCC AGT ACC AGA TCT		110
Gln Thr Gln Lys Leu Pro Ser Phe Ala Leu Pro Pro MET Ala Ser Thr Arg Ser		
CCT AAG TTC TAC ATG GCC TCT ACC CTC AAG TCT GGT TCT AAG GAA GTT GAG AAT		164
Pro Lys Phe Tyr MET Ala Ser Thr Leu Lys Ser Gly Ser Lys Glu Val Glu Asn		
CTC AAG AAG CCT TTC ATG CCT CCT CGG GAG GTA CAT GTT CAG GTT ACC CAT TCT		218
Leu Lys Lys Pro Phe MET Pro Pro Arg Glu Val His Val Gln Val Thr His Ser		
ATG CCA CCC CAA AAG ATT GAG ATC TTT AAA TCC CTA GAC AAT TGG GCT GAG GAG		272
MET Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Asp Asn Trp Ala Glu Glu		
AAC ATT CTG GTT CAT CTG AAG CCA GTT GAG AAA TGT TGG CAA CCG CAG GAT TTT		326
Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe		
TTG CCA GAT CCC GCC TCT GAT GGA TTT GAT GAG CAA GTC AGG GAA CTC AGG GAG		380
Leu Pro Asp Pro Ala Ser Asp Gly Phe Asp Glu Gln Val Arg Glu Leu Arg Glu		
AGA GCA AAG GAG ATT CCT GAT GAT TAT TTT GTT GTT TTT GGA GAC ATG ATA		434
Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile		
ACG GAA GAA GCC CTT CCC ACT TAT CAA ACA ATG CTG AAT ACC TTG GAT GGA GTT		488
Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val		

FIGURE 3B
1 of 3

CGG GAT GAA ACA GGT GCA AGT CCT ACT TCT TGG GCA ATT TGG ACA AGG GCA TGG Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Thr Trp Ala Ile Trp Thr Arg Ala Trp	542
ACT GCG GAA GAG AAT AGA CAT GGT GAC CTC CTC AAT AAG TAT CTC TAC CTA TCT Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser	596
GGG CGA GTG GAC ATG AGG CAA ATT GAG AAG ACA ATT CAA TAT TTG ATT GGT TCA Gly Arg Val Asp MET Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser	650
GGG ATG GAT CCA CGG ACA GAA AAC AAG CCA TAC CTT GGG TTC ATC TAT ACA TCA Gly MET Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser	704
TTC CAG GAA AGG GCA ACC TTC ATT TCT CAT GGG AAC ACT GCC CGA CAA GCC AAA Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys	758
GAG CAT GGA GAC ATA AAG TTG GCT CAA ATA TGT GGT ACA ATT GCT GCA GAT GAG Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu	812
AAG CGC CAT GAG ACA GCC TAC ACA AAG ATA GTG GAA AAA CTC TTT GAG ATT GAT Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp	866
CCT GAT GGA ACT GTT TTG GCT TTT GCT GAT ATG ATG AGA AAG AAA ATT TCT ATG Pro Asp Gly Thr Val Leu Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET	920
CCT GCA CAC TTG ATG TAT GAT GGC CGA GAT GAT AAT CTT TTT GAC CAC TTT TCA Pro Ala His Leu MET Tyr Asp Gly Arg Asp Asp Asn Leu Phe Asp His Phe Ser	974

FIGURE 3B
2 of 3

GCT GTT GCG CAG CGT CTT GGA GTC TAC ACA GCA AAG GAT TAT GCA GAT ATA TTG Ala Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu	1028
GAG TTC TTG GTG GGC AGA TGG AAG GTG GAT AAA CTA ACG GGC CTT TCA GCT GAG Glu Phe Leu Val Gly Arg Trp Lys Val Asp Lys Leu Thr Gly Leu Ser Ala Glu	1082
GGA CAA AAG GCT CAG GAC TAT GTT TGT CGG TTA CCT CCA AGA ATT AGA AGG CTG Gly Gln Lys Ala Gln Asp Tyr Val Cys Arg Leu Pro Pro Arg Ile Arg Arg Leu	1136
GAA GAG AGA GCT CAA GGA AGG GCA AAG GAA GCA CCC ACC ATG CCT TTC AGC TGG Glu Glu Arg Ala Gln Gly Arg Ala Lys Glu Ala Pro Thr MET Pro Phe Ser Trp	1190
ATT TTC GAT AGG CAA GTG AAG CTG TAGGTGGCTA AAGTGCAGGA CGAAACCGAA ATGGTTAGTT Ile Phe Asp Arg Gln Val Lys Leu	1254
TCACCTCTTTT TCATGCCCAT CCTGCAGAA TCAGAAGTAG AGGTAGAATT TTGTAGTTGC TTTTTTATTA	1324
CAAGTCCAGT TTAGTTTAAG GTCTGTGGAA GGGAGTTAGT TGAGGAGTGA ATTAGTAAG TTGTAGATAC	1394
AGTTGTTTCT TGTGTTGTCA TGAGTATGCT GATAGAGAGC AGCTGTAGTT TTGTTGTGT GTTCTTTTAT	1464
ATGGTCTCTT GTATGAGTTT CTTTCTCTTC CTTTCTCTCT TTCCCTTTCCT CTCTCTCTCT CTCTCTCTCT	1534
CTCTTTTCTT CTTATCCCCA GTGTCTCAAG TATAATAAGC AAACGATCCA TGTGGCAATT TTGATGATGG	1604
TGATCAGTCT CACAACCTGA TCTTTTGTCT TCTATTGGAA ACACAGCCTG CTTGTTTGAA AAAA	1668

FIGURE 3B
3 of 3

1 TGAGAGATAGTGTGAGAGCATTAGCCTTAGAGAGAGAGAGAGAGCTTGTGTCTGAAAGAATCCACAA 69

HindIII

70 ATGGCATTGAAGCTTAACCCCTTTGGCATCTCAGCCTTACAACCTTCCCT 117
METAlaLeuLysLeuAsnProLeuAlaSerGlnProTyrAsnPhePro

FIGURE 4A

PstI |
 1 ACTTCATGGGCTATTTGGACAAGAGCTTGGACTGCAGAAAGAGAACCGACACGGTGATCTTCTCAATAAG 69
 ThrSerTrpAlaIleTrpThrArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuAsnLys

 70 TATCTTTACTTGTCTGGACGTGTTGACATGAGGCAGATTGAAAAGACCATTTCAGTACTTGATTGGTTCT 138
 TyrLeuTyrLeuSerGlyArgValaspMETArgGlnIleGluLysThrIleGlnTyrLeuIleGlySer

 BamHI |
 139 GGAATGGATCCTAGAAACAGAGAAACAATCCTTACCTCGG 176
 GlyMETaspProArgThrGluAsnAsnProTyrLeuAla

FIGURE 4B

TGAGAGATAG TGTGAGAGCA TTAGCCTTAG AGAGAGAGAG AGAGAGCTTG TGTCTGAAAG AATCCACAA

ATG GCA TTG AAG CTT AAC CCT TTG GCA TCT CAG CCT TAC AAC TTC CCT TCC TCG
MET Ala Leu Lys Leu Asn Pro Leu Ala Ser Gln Pro Tyr Asn Phe Pro Ser Ser

GCT CGT CCG CCA ATC TCT ACT TTC AGA TCT CCC AAG TTC CTC TGC CTC GCT TCT
Ala Arg Pro Pro Ile Ser Thr Phe Arg Ser Pro Lys Phe Leu Cys Leu Ala Ser

TCT TCT CCC GCT CTC AGC TCC AAG GAG GTT GAG AGT TTG AAG AAG CCA TTC ACA
Ser Ser Pro Ala Leu Ser Ser Lys Glu Val Glu Ser Leu Lys Lys Pro Phe Thr

CCA CCT AAG GAA GTG CAC GTT CAA GTC CTG CAT TCC ATG CCA CCC CAG AAG ATC
Pro Pro Lys Glu Val His Val Gln Val Leu His Ser MET Pro Pro Gln Lys Ile

GAG ATC TTC AAA TCC ATG GAA GAC TGG GCC GAG CAG AAC CTT CTA ACT CAG CTC
Glu Ile Phe Lys Ser MET Glu Asp Trp Ala Glu Gln Asn Leu Leu Thr Gln Leu

AAA GAC GTG GAG AAG TCG TGG CAG CCC CAG GAC TTC TTA CCC GAC CCT GCA TCC
Lys Asp Val Glu Lys Ser Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser

GAT GGG TTC GAA GAT CAG GTT AGA GAG CTA AGA GAG AGG GCA AGA GAG CTC CCT
Asp Gly Phe Glu Asp Gln Val Arg Glu Leu Arg Glu Ala Arg Glu Leu Pro

GAT GAT TAC TTC GTT GTT CTG GTG GGA GAC ATG ATC ACG GAA GAG GCG CTT CCG
Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile Thr Glu Glu Ala Leu Pro

FIGURE 4C
1 of 3

ACC TAT CAA ACC ATG TTG AAC ACT TTG GAT GGA GTG AGG GAT GAA ACT GGC GCT
 Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 AGC CCC ACT TCA TGG GCT ATT TGG ACA AGA GCT TGG ACT GCA GAA GAG AAC CGA
 Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg
 CAC GGT GAT CTT CTC AAT AAG TAT CTT TAC TTG TCT GGA CGT GTT GAC ATG AGG
 His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Ser Gly Arg Val Asp MET Arg
 CAG ATT GAA AAG ACC ATT CAG TAC TTG ATT GGT TCT GGA ATG GAT CCT AGA ACA
 Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly MET Asp Pro Arg Thr
 GAG AAC AAT CCT TAC CTC GGC TTC ATC TAC ACT TCA TTC CAA GAA AGA GCC ACC
 Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr
 TTC ATC TCT CAC GGA AAC ACA GCT CGC CAA GCC AAA GAG CAC GGA GAC CTC AAG
 Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His Gly Asp Leu Lys
 CTA GCC CAA ATC TGC GGC ACA ATA GCT GCA GAC GAG AAG CGT CAT GAG ACA GCT
 Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala
 TAC ACC AAG ATA GTT GAG AAG CTC TTT GAG ATT GAT CCT GAT GGT ACT GTG ATG
 Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val MET
 GCG TTT GCA GAC ATG ATG AGG AAG AAA ATC TCG ATG CCT GCT CAC TTG ATG TAC
 Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET Pro Ala His Leu MET Tyr

FIGURE 4C
 2 of 3

GAT GGG CGG GAT GAA AGC CTC TTT GAC AAC TTC TCT TCT GTT GCT CAG AGG CTC
 Asp Gly Arg Asp Glu Ser Leu Phe Asp Asn Phe Ser Val Ala Gln Arg Leu
 GGT GTT TAC ACT GCC AAA GAC TAT GCG GAC ATT CTT GAG TTT TTG GTT GGG AGG
 Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg
 TGG AAG ATT GAG AGC TTG ACC GGG CTT TCA GGT GAA GGA AAC AAA GCG CAA GAG
 Trp Lys Ile Glu Ser Leu Thr Gly Leu Ser Gly Glu Asn Lys Ala Gln Glu
 TAC TTG TGT GGG TTG ACT CCA AGA ATC AGG AGG TTG GAT GAG AGA GCT CAA GCA
 Tyr Leu Cys Gly Leu Thr Pro Arg Ile Arg Arg Leu Asp Glu Arg Ala Gln Ala
 AGA GCC AAG AAA GGA CCC AAG GTT CCT TTC AGC TGG ATA CAT GAC AGA GAA GTG
 Arg Ala Lys Lys Gly Pro Lys Val Pro Phe Ser Trp Ile His Asp Arg Glu Val
 CAG CTC TAA AAAGGAA CAAAGCTATG AAACCTTTTC ACTCTCCGTC GTCCCTCATT TGATCTATCT
 Gln Leu *
 GCTCTTGAAA TTGGTGTAGA TTA CTATATGGT TTGTGATATT GTTCGTGGGT CTAGTTACAA AGTTGAGAAG
 CAGTGATTTA GTAGCTTTGT TGT TTCCAGT CTTTAAATGT TTTTGTGTTT GGTCCTTTTA GTAAACTTGT
 TGTAGTTAAA TCAGTTGAAC TGTTTGGTCT GT

FIGURE 4C
 3 of 3

GAT GCC AAA ANG CCT CAC ATG CCT CCT AGA GAA GCT CAT GTG CAA AAG	48
Asp Ala Lys Xaa Pro His MET Pro Pro Arg Glu Ala His Val Gln Lys	15
	10
	5
	1
ACC CAT TCA ATK CCG CCT CAA AAG ATT GAG ATT TTC AAA TCC TTG GAG	96
Thr His Ser Xaa Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Glu	30
	25
	20
GGT TGG GCT GAG GAG AAT GTC TTG GTG CAT CTT AAA CCT GTG GAG AA	143
Gly Trp Ala Glu Glu Asn Val Leu Val His Leu Pro Val Glu	45
	40
	35

FIGURE 5

**Amino Acid
Sequence From
Fragment F2**

K	E	I	P	D	D	Y	FVVLVGDMITEEALPTY	Q	T	M	L	N	T
AAA	GAA	AUU	CCN	GAU	GAU	UAU		CAA	ACN	AUG	CUN	AAU	AC/N
G	G	C	C	C	C	C		G				C	

A

Forward Primers:

5'GCTAAGCTT AAP GAP ATQ CA GAQ GAQ TA3' Desat 13-1
 A CCG Desat 13-2
 CCC Desat 13-3
 CCT Desat 13-4

**Reverse Primers:
(complements)**

Desat 13-5a 3' GTQ TGN TAC GAN TTP TGCTTAAGCGA 5'
 Desat 13-6a AAQ

Oligonucleotides

P = A or G
 Q = T or C
 N = A, C, T or C

FIGURE 6

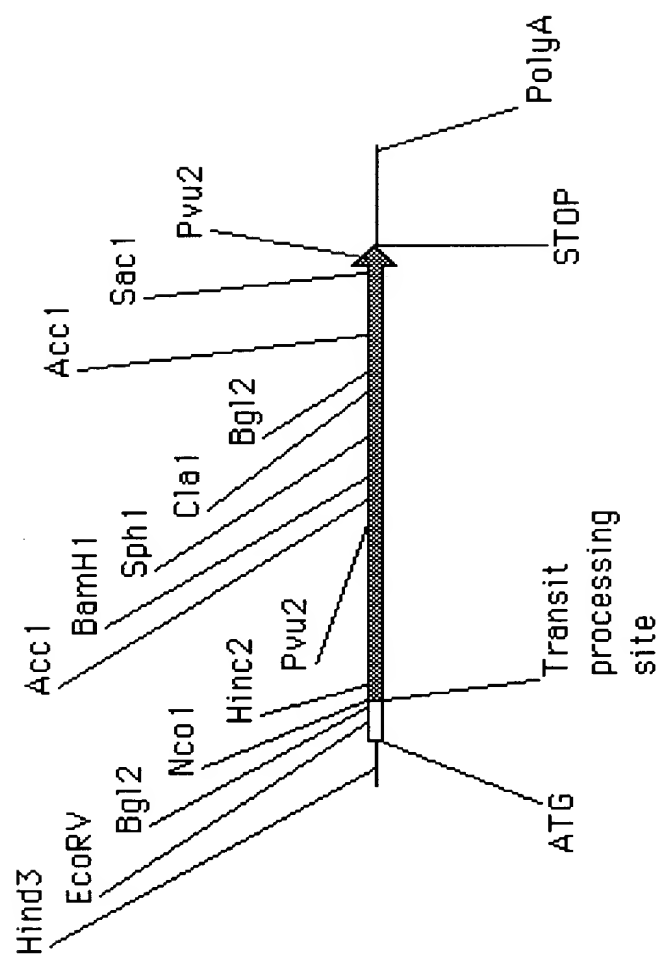


FIGURE 7A

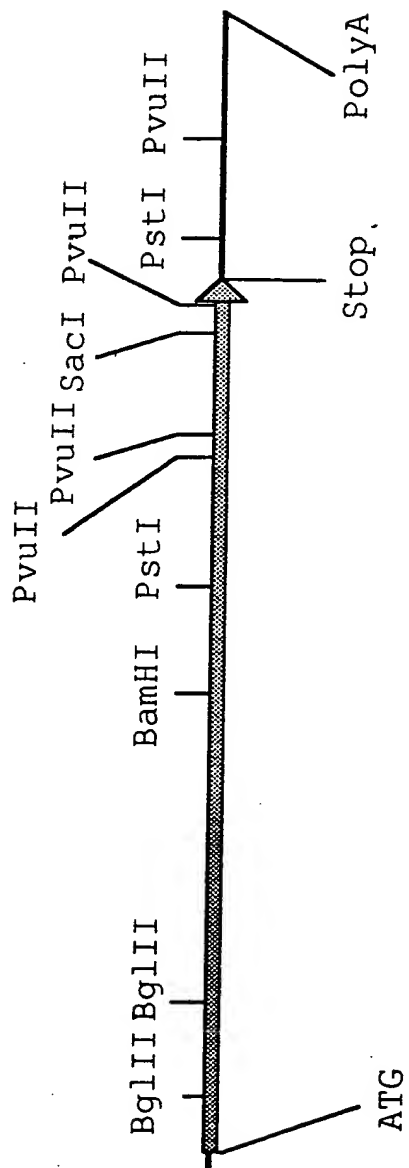


FIGURE 7B

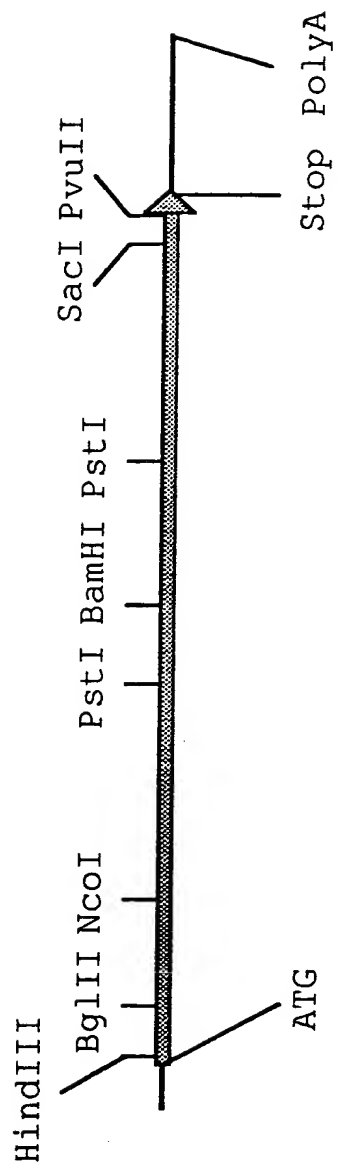


FIGURE 7C

TCTAGAAATTC	TCTAATTACG	TCTGTTTGTT	CTATTTTTTA	TATGATATCA	AATATTCTGC	ATAAAATATAT	70
GGTTTAAGAT	GCCAAAAAAT	TATTTACTTG	GTGAATATAA	TACGTTAAAT	ATTAGAAATA	CATCATTTAG	140
TTAAATAAAT	AACCAAAAAC	CAAAAATCA	TATCCGCGCT	GGCGCGCGGT	CAGGGTCTCG	TTAGTTTTAA	210
AATCAATGCA	GTTTACAATT	AATTTCCAGC	TGAAAAATAAG	TATAATTTGT	ATTGAAAATTA	TAAAGTGACA	280
TTTTTTGTGT	AACAAATATT	TTGTGTAAAC	AGAAATTAAAA	AAAAAAACAG	AAAATACTCA	GCTTTTTTAA	350
TAATAAAAAA	AATTAATTGA	GTTAGAAAAAT	TGTTGTACCA	ATAACAAAAG	ATTTATATGG	AATTATAAAA	420
TCAACACACC	AATAACACAA	GACTTTTTTAA	AAATTTAAGA	ATAATATAAG	CAATAACAAT	AGAATCTTCA	490
AATTCTTCAA	ATCCTTAAAA	ATCAATCTCC	CACTATTAAT	CCCCCTTAGT	TTTAGTTGGT	AATGGCAACG	560
TTTGTGACT	ACCGTATTGT	AACTTTGTG	AAATTGTCT	AAATACGTGT	CAAACTCTGG	TAAAAAATTA	630
GTCTGTACA	TCTGTCTTTT	ATTATAAAAA	CACAGCTGTT	AATCAGAATT	TGGTTTATTA	AATCAACAAC	700
CTGCACGAAA	CTTGTGTGAG	CATATTTTGT	CTGTTTCTGG	TTCATGACCT	TCTTCCGCAT	GATGGCCAAG	770
TGTAATGGCC	ACTTGCAAGA	GCGTTTCTTC	AACGAGATAA	GTCGAACAAA	TATTTGTCCG	TTACGACCAC	840
ATATAAAATC	TCCCCATCTC	TATATATAAT	ACCAGCATTC	ACCATCATGA	ATACCTCAAA	TCCCAATCTC	910
ACAAATACTT	CAATAAAAAAG	ACCAAAAAAAA	ATTAAAGCAA	AGAAAAGCCT	TCTTGTGCAC	AAAAAAAAAAA	980

GAAGCCTTCT AGGTTTTCAC GAC ATG AAG TTC ACT ACT CTA ATG GTC ATC ACA TTG 1036
 MET Lys Phe Thr Thr Leu MET Val Ile Thr Leu
 GTG ATA ATC GCC ATC TCG TCT CCT GTT CCA ATT AGA GCA ACC ACG GTT GAA AGT 1090
 Val Ile Ile Ala Ile Ser Ser Pro Val Pro Ile Arg Ala Thr Thr Val Glu Ser
 TTC GGA GAA GTG GCA CAA TCG TGT GTT GTG ACA GAA CTC GCC CCA TGC TTA CCA 1144
 Phe Gly Glu Val Ala Gln Ser Cys Val Val Thr Glu Leu Ala Pro Cys Leu Pro
 GCA ATG ACC ACG GCA GGA GAC CCG ACT ACA GAA TGC TGC GAC AAA CTG GTA GAG 1198
 Ala MET Thr Thr Ala Gly Asp Pro Thr Thr Glu Cys Cys Asp Lys Leu Val Glu
 CAG AAA CCA TGT CTT TGT GGT TAT ATT CGA AAC CCA GCC TAT AGT ATG TAT GTT 1252
 Gln Lys Pro Cys Leu Cys Gly Tyr Ile Arg Asn Pro Ala Tyr Ser MET Tyr Val
 ACT TCT CCA AAC GGT CGC AAA GTC TTA GAT TTT TGT AAG GTT CCT TTT CCT AGT 1306
 Thr Ser Pro Asn Gly Arg Lys Val Leu Asp Phe Cys Lys Val Pro Phe Pro Ser
 TGT TAAATCTCTC AAGACATTGC TAAGAAAAAAT ATTATTAAAA ATAAAAAGAAT CAAACTAGAT 1369
 Cys
 CTGATGTAAC AATGAATCAT CATGTTATGG TTGAAGCTTA TATGCTGAAG TGTTTGATTT TATATATGTG 1439
 TGTGTGTGTG TCCTGCTCAA TTTTGTGAAAC ACACACGTTT CTCCTGATTT GGATTTAAAT TATATTTTGA 1509
 GTTAAAAAAA AGAAAAAGAT GGAATGCTAT TTATACAAGT TGATGAAAAA GTGGAAGTAC AATTAGATA 1579

TCTCCTACAC TTAAGAATG AAACAATAAT AACTTACGA AACAAATGAA AAATACATAA ATTGTCGACA 1649
ATCAACGTCC GATGACGAGT TTATTATTAA AAATTGTGT GAAGGACTAG CAGTTCAACC AAATGATATT 1719
GAACATATAC ATCAACAAAT ATGATAATCA TAAAAGAGAG AATGGGGGGG GGGTGTCTGT TACCAGAAAC 1789
CTCTTTTCT CAGCTCGCTA AAACCCCTACC ACTAGAGACC TAGCTCTGAC CGTCGGCTCA TCGGTGCCGG 1859
AGGTGTAACC TTTCTTTCCC ATGACCCGAA ACCTCTCTTT CCCAACTCAC GAAAACCCCTA CAATCAAAAA 1929
CCTAGCTCCG ACCGTCGGCT CATCGGTGCC GAAGGTGTAA CCTTCTCTC CCATCATAGT TTCTCGTAAA 1999
TGAAAGCTAA TTGGGCAATC GATTTTTTAA TGTTTAAACC ATGCCAAGCC ATTTCTTATA GGACAATTGT 2069
CAATAATAGC ATCTTTTGAG TTTTGTCTCA AAAGTGACAC TAGAAGAAAA AGTCACAAA AATGACATTG 2139
ATTAAAAAGT AAAATATCCC TAATACCTTT GGTTTAAATT AAATAAGTAA ACAAAAATAA ATAAAAACAA 2209
ATAAAATAAA AATAAAAAAT GAAAAAAAAGA AATTTTTTAA TAGTTTCAGA TTATATGTTT TCAGATTCTGA 2279
AATTTTTTAA ATCCCTTTT TTAAATTTTC TTTTTTGAAA TTTTTTTTTT TGAAATTTTT TGAAACTGTT 2349
TTTAAAAATT TTATTTTTAA TTTTTTTAGTA TTTATTTTTT ATTTTATAAA ATTTTAAACG CTAATTCCAA 2419
AACTCCCCC CCCCCCCCCC CCCCATTCT CTCCTAGTCT TTTTCTCTCTT CTATATTTG GGCCTCTATC 2489
TTCTCTTTT TTTTCAGGCC CAAAGTATCA TGTGTAACAA CCGGTGTTCA AAAACGGCC CGCCTGGCCG 2559

TTTACTCGCC CGATTAAATG ATGATCGGAA GGCTGCCATG GCGAGGCGGA GGTAATCAGT GGTTCCTAGGC 2629
 GCTGAAACTA GAAAAACCTTC AAAAAATCGAA ATTTTAAAGAG CTAAATCGGT GTTTATCTCA TGAATCTATT 2699
 ATATTTAGTT GAAACTCACA AGAATCGGTT GTAAAAACTA TGAATCGTG CAAAAAAT GAAAGAACAAA 2769
 ATATTCTCAG ATCTGGAAAA CACAGAGAAG AGGTGAAGA TGAGGGTAAA ATCGTATTTT GTCATTTCAAT 2839
 AAACTAAAAAT CAAAAAATAA TGATGCAAAA TTCAATGATA ATAACTCGAA CTCGCAACCA TATGCATCTT 2909
 TAGACTGCGA CACGGACCAC TAGACTAAGC AATTTTAAATG TTTATTTCATC ACAGACCTAA TATATGTCTA 2979
 AAACTAGGCG CCGAGTACGC CCCGCTTAAT CCCGAGTTTT TGTTAGCTCG CTAGACCCAG GGTCAACCGCC 3049
 CGACTAACGA GTAGCGTAAT TCTGAACTGG GGTAAACAACA TAGAGAACAT CGCCGACCCT TCCCTGCCGA 3119
 TGATGCCGCC TCCGATGAAC TTCCCTGTAAC GCCTTCAGTT TCCATTGATT TTCCCCCTTTA ATCTGATCAG 3189
 TTCCATGTTT TATCCAACTC ATCCCACTCC GTAGCATTTA ATCGATCTCA TCATTTACAT ACATAACCAG 3259
 TAGGAGGTCT CATAATAATT TGAACGTTTC CAGCGATGAA CAGTGCCAAT CTCTGCGAAA TCCATTTCTC 3329
 TAAAGCTCAGG GCTGGCGGCT GCAGCCCCGG GATCCACTAG TTCTAGGCGG CCGCACCGCG GTGGAGCTCC 3399
 AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG C 3440

CTCGAGAGCT GAAGGATTTT TTGTTAGAGA TTCAACGACA GATGGACCCT TCCTCCACTA 60
 GGCAACTGCA AGAACCTAAC AATGCAAATA TCACTCCTCC TCAGCCTTCA AGGAGCGTTA 120
 ATAGGACTGG AACAAAGCGGT CAAGTGAGTA AATTTTCCTT CCAAGATAGA TCTCTATCGT 180
 TCGGTTCATG AAGTTTGTGG TTAAATTGTG TAGCAACAGG ATAGTGCAAG TGAGAATAGA 240
 GTTCGACCTC ATCTACCTAC CCCGGAACCT CTGAATGTAT CCCCATTTGAA GAAGAAGAGG 300
 GCAAATCCTG CACCCAGAAG GATAAAGAAA TTTTGGACGC CTGAAGAAGT GGCAGTTCTG 360
 AGGGAAGGAG TAAAAGAGTA TGTCTACTAC TACTACTCTA TAATCAAGTT TCAAGAAGCT 420
 GAGCTTGGCT CTCACTTTAT ATGTTTGATG TTGTTGTGCA GGTATGGTAA ATCATGGAAA 480
 GAGATAAAGA ATGCAAACCC TGAAGTATTG GCAGAGAGGA CTGAGGTGAG AGAGCATGTC 540
 ACTTTTGTGT TACTCATCTG AATTATCTTA TATGCGAATT GTAAAGTGGTA CTAAAAGGTT 600
 TGTAACTTTT GGTAGGTGGA TTTGAAGGAT AAATGGAGGA ACTTGCTTCG GTAGCGGTAA 660
 CAAGTTTTAT ATTGCTATGA AGTTTTTTTG CCTGCGTGAC GTATCAGCAG CTGTGGAGAA 720
 GATGGTATTA GAAAGGGTCT TTTCACATTT TGTGTTGTGA CAAATATTAA TTCGGCCGGT 780
 ATGGTTTGGT TAAGACTTGT TGAGAGACGT GTGGGGTTTT TTGATGTATA ATTAGTCTGT 840
 GTTTAGAACG AAACAAGACT TGTTCGTAT GCCTTTTTTA ACTTGAGGGG GTTTGTGTGT 900
 GTTAGTTAGG AACTTGACTT TGTCTCTTTC TCTCAAGATC TGATTGGTAA GGTCTGGGTG 960
 GTAGTACTGT TTGGTTTAAT TTGTTTGTGAC TATTGAGTCA CTGTGGCCCA TTGACTTTAA 1020

FIGURE 9
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ATTAGGCTGG TATATTTTTT GGTTTAAAC CGGTCTGAGA TAGTGCAATT TCGATTCAAGT 1080
CAATTTTAAA TTCTTCAAGG TAATGGGCTG AATACTTGTA TAGTTTAAAG ACTTAACAGG 1140
CCTTAAAGG CCCATGTTAT CATAAAACGT CATTTGTTTAG AGTGCACCAA GCTTATAAAA 1200
TGTAGCCAGG CCTTAAAGA CTTAACAGGC CTTAAAAGAC TTAACATTCC TTAAGAGGCC 1260
CATGTTATCA TAAAACGTCA TCGTTTTGAG TGCACCAAGC TAAATGTAGC CAGGCCTTAA 1320
AAGACTTAAC AGGCCTTAA AGGCCCATGT TATCATAAAA CGCCGTCGTT TTGAGTGCAC 1380
CAAGCTTATA AATGTAGCCA GCTACCTCGG GACATCACGC TCCTTGTAACA CTCGCCCATC 1440
TCTCTCTCTC TCGAGCAGAT CTCTCTCGG AATATCGACA ATGTCGACCA CTTTCTGCTC 1500
TTCCGCTCTC ATGCAAGCCA CTCTCTGGT AATCTCATCT CCTTCTTGTG TTCCCAGATC 1560
GCTCTGATCA TACTTTCTTT TAGATCATTT GCCTCTGATC TGTTGCTTGA TGTTTGTAA 1620
CTCTCCACGC ATGTTTGATT ATGTTGAGAA TTAGAAAAAA AATGTTAGCT TTACGAAATCT 1680
TTAGTGATCA TTTCAATTGG ATTTGCAATC TTGTGTGACA TTTGAGGCTT GTGTAGATTT 1740
CGATCTGTAT TCATTTTGAA TCACAGCTAT AATAGTCATT TGAGTAGTAG TGTTTATAAA 1800
TGAACATGTT TTGTTGTATT GATGGAACAA ACAGGCAGCA ACAACGAGGA TTAGTTTCCA 1860
GAAGCCAGCT TTGGTTTCAA CGACTAATCT CTCCTTCAAC CTCGCCCGTT CAATCCCCAC 1920
TCGTTTCTCA ATCTCCCTGG CGGTATGTTT TCATTCTCAG CATTATTTT GAGCTTGCTT 1980
GTCATGGTAC TCTCTCTAAT TGTCTATTG GTTTATTAGG CCAAAACCAGA GACGGTTGAG 2040

AAAGTGTCTA AGATAGTTAA GAAGCAGCTA TCACTCAAAG ACGACCAAAA GGTCGTGCG 2100
GAGACCAAAGT TTGCTGATCT TGGAGCAGAT TCTCTCGACA CTGTAAGTCA TCAATCATTC 2160
TCTTATGTGA ATAAAGAGAA CTTGAAGAGT TTGTTTTTAA CATATTAAC T GAGTGTTTTG 2220
CATGCAGGTT GAGATAGTGA TGGGTTTAGA GGAAGAGTTT GATATCGAAA TGGCTGAAGA 2280
GAAAGCTCAG AAGATTGCTA CTGTGGAGGA AGCTGCTGAA CTCATTGAAG AGCTCGTTCA 2340
ACTTAAGAAAG TAATTTTAGT ATTAAGAGCA GCCAAGGCTT TGTGGGTTT GTTGTTTTCA 2400
TAATCTTCCT GTCATTTTCT TTTTCTTTAA TGTGTCAAGC GACTCTGTG GTTTAAAGTA 2460
GTATCTGTTT GCCATGGATC TCTCTCTATT TGTCGACTGA AAACTTTTGG TTACACATG 2520
AAAGCTTGTT CTGTCTCTT CTAAATCGA AATGCCAAAT GCGAGATTAG GGAATCTTGT 2580
ATTAACACAT ACATAAGTCA AAGAGTAGGC CCTAAGATGA CAATTTATAA ACAATCCTAT 2640
TCACATTGTA TATACAGGTT ATGATTATT CCAATCAGCG TCAAGAATC CAGCATCTTT 2700
CATCTCTGAA TAGTAGACAT TCTCCAAGTT CACATCTTCC TCCTGCACCA AAAACCCAGTA 2760
CTAAATCATG AACATTGCAA TAATCACATG CCTAGGCGAG AGTTTTGGTG ATGTGGTGT 2820
AGTGATAGTG ATACTGATGG TGCTAGAGCG GTTAAGAAGG ATTAACCTGG AAGAAGTCTG 2880
CAAGGAAAGT AACATAGAGA AGAGGAAGAT AGGAGTGGA ACAAAACACTT GTGATCCCAT 2940
ACAGCCTCCC AGCATTTTTC AAATGTTATT TCCTTACATA AAGAAACAAG AGAAGTCTGA 3000
CTAGATGATA TTTATATAGG ATAAGTGT TT TACCATAAGC CAAAGTGAGC GCCGTTTGCA 3060

AGAGCTAAAC AGACAGTACA CGTTTGGCAT ATATCTCATC AACATGATCT GAAAAAGTAAC 3120
ATATCACAGT TAATGAACAC AATGGTTACC TTGAGAAAGCA AATCAAGACC TATAACAAGC 3180
CCAGAGATGA GAAAGTCCG TGTCAACGCT TCACCGCCAT TCGCGTAGTT TCCTTGGAAG 3240
ACAAAGGCCA CCAACCAAAC TTACTIONCAG AAACAACACT CCAAAATGTTG TCAACAAAAGT 3300
CAATAGATTC CAAACTACTT CGTTACAGGG TTGTATAGAT AATAATAATAG AATAGTGGGA 3360
AGATAGTATA AATAAAATAA ATAAAAGATC CTATCGGTAA ATAGTTTATA ATATCGGGG 3420
CGTATATAAA GTATAAAAGA AACTCTTCTC CAATCCGACC GTTGAAAATC ACTCTCAATC 3480
TCTGGCGTAA CGACCGGATC GTTCGCGCGT AATTTCGCT GCTATAAATA GAAACTTTCC 3540
TCTTCTGTTT CTCGATCAA ATTTTTTTTT GGAAAAATTA AGTTTGAATC TATCGTAGAT 3600
GCTGTGACAA AAAAAAATTG TTTTATCGAA GATGAGAAAC ATGAGGCCCTG TTCATGCAAG 3660
GAACCAGACC ACGGATCCAT CTTCCGCCGAT GATGACGTCT CCTCTGATGA ATCGTCACGC 3720
ACGGACAGGA TCCAACGCTG GACCAGCATC TAACGCCAAG AAAGCACAGA CGAAAGCAGC 3780
AGCTCAGAGA CTCGCGGCTG TGATGTCGAA CCAAAACAGGC GACGATGAAG ACAGTGATGA 3840
TGACCTTTCC TTTGACTACA ACGCTGTCGG AAGCATTTGT CTCGCTGCCG GAAGATCT 3898

Lambda CGN1-2

NCG-186 Linear

LENGTH = 4325

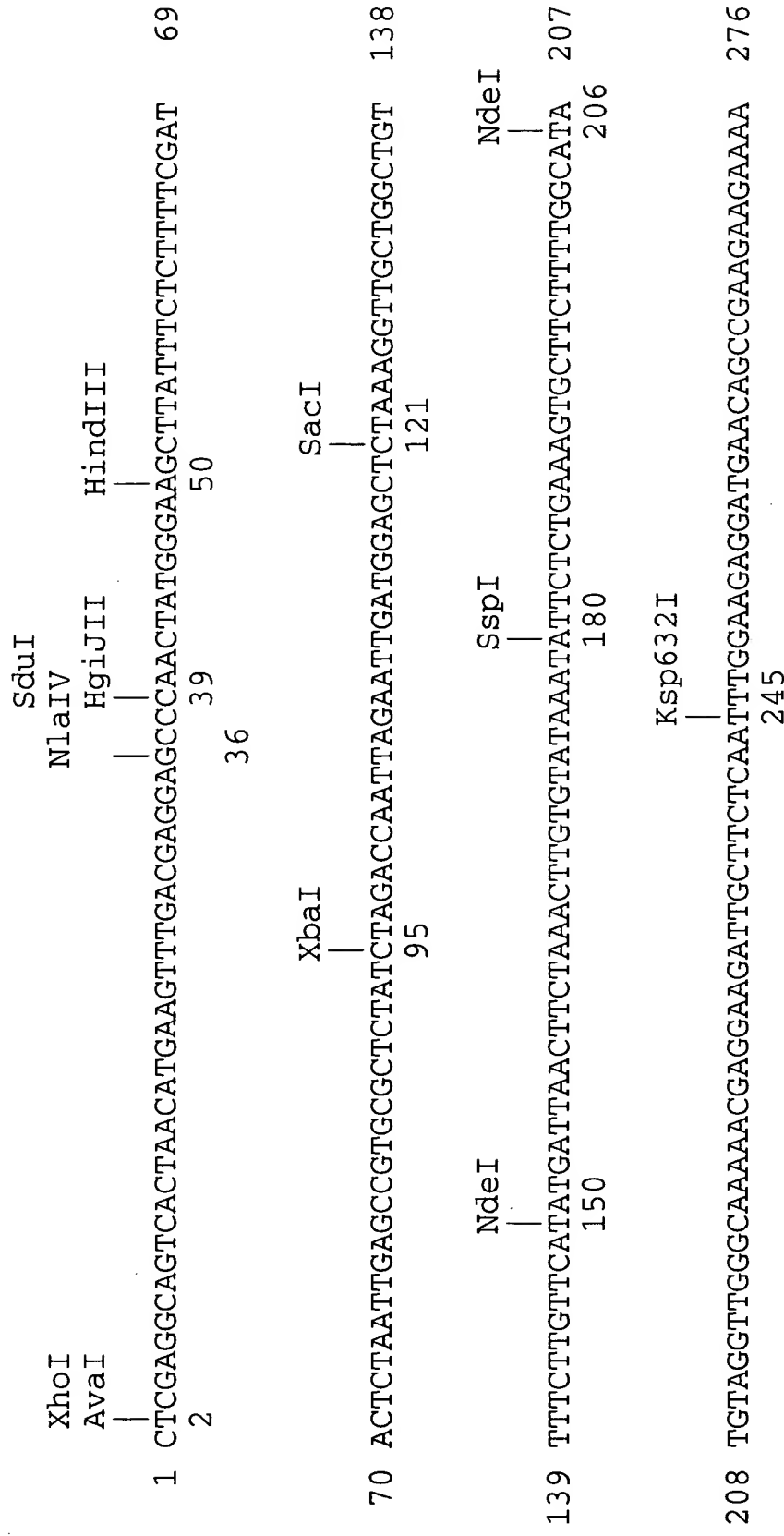


FIGURE 10

XhoII
 277 TAAGAATAGGCAGTCCTGCTACTCAATGATCTCAGTCTATAACGGTCGTCGTCATGAAACAGAGGT 345
 305
 MmeI EcoRV
 346 AAAACATTTTTCATATACACTTTGAAAGTTCCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414
 401 408
 SduI
 MstI
 BclI HgiAI
 415 CAATGTCGGAGAGACAA3GGCTGMNCANCATATACAAAAGGGAATGAAGATGGCCTTTTGATTAGCTG 483
 437 442
 439
 HaeI
 469
 SduI
 HgiJII
 484 TGATGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACCTGGATTCACTTCTCAAGTTTA 552
 512

FIGURE 10
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Cfr10I
 BbvII
 553 TGAGTTGTCACCCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAAATCAATTTGATTTGT 621
 560
 563
 622 AGTAAACTAAGAAGAACTTACCTTATGTTTTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAAGAAC 690
 SacI
 691 TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTGTCAAAAGGTTAGTGT 759
 731
 BbvII
 760 TTAGTGAATAATAAACTTATACCAACAAGTCTTTCATTGACTTATTTATATACTTGTGTGAATTGCTAG 828
 782
 829 GAACTACTTATTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT 897
 898 GGAAAGAAGATTTTCATGTAAACCTCCATGACAACCTGCTGGTAATCGTTGGGGTGTGTAATGTCGAGGA 966
 BclI
 967 ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTATATTTTCCCTGATAGT 1035
 981

1036 CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGAGCTTGACTTTTGTACCCAAAGCGATGGGATAC 1104

1105 ATAGGAGGTGGGAGAAATGGGTATAGAAATAACATCAATGGCAGCAACTGCCGATCAAGCAGCTTTCATAT 1173

Tth1111II
|
1174 TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCTCAAGTA 1242
1175

XhoII
|
1243 CTCATGTCAAGGTGGTTTCCTTAGCTTTGAACACAGATTTGGATCTTTTGTGTTTGTTCATATACT 1311
1285

1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTCAGGACAAAATGGGCGAAGAATCTGTACATTTGCATCA 1380

AflII
|
1381 ATATGCTATGGCAGGACAGTGTGCTGTATACACACTTAAAGCATCATGTGGAAGCCAAAGACAAATTGGAG 1449
1415

1450 CGAGACTCAGGTCGTCAATAATACCAATCAAAGACGTAAACCAGACGCAACCTCTTTGGTTGAATGTA 1518

SspI
|
1519 ATGAAAGGGATGTGTCTTGGTATGTATGTACGAATAACAAAAGAGAAGATGGAATTAGTAGTAAAAATA 1587
1587

FIGURE 10
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1588 TTTGGGAGCTTTTAAAGCCCTTCAAGTGTGCTTTTATCTTATGATATCATCCATTTCGTTGTTAA 1656
 EcoRV
 1635
 1657 TGCCTCTCTAGATATGTTCCCTATATCTTTCAGTGTCTGATAAGTGAGAAAAACCATACCAA 1725
 XbaI
 1664
 1726 ACCAAAAATATTCAAATCTTATTTTAAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG 1794
 SspI
 1789
 1795 TGCTGAATCTATCACACTAGAAAAAACATTTCTCAAGGTAATGACTTGTGGACTATGTTCTGAAATTC 1863
 EcoRI
 1859
 1864 TCATTAAAGTTTATTTTCTGAAGTTTAAAGTTTACCTTCTGTGTTTTGAAAATATATCGTTCATAAGATG 1932
 Eco57I
 1904

1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTGTCACTCACTTCAA 2001
 SphI
 NspI
 1971

2002 CACCTAAGAGCTTCTCTCACAGCGCACACACATATGCATGCAATATTACACGTGATCGCCATGCAA 2070
 Tth111II
 NdeI SphI PmaCI
 [AvaIII] SspI AflIII
 2015 2037 2048 2053
 2036 2044 2056

2071 ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAACCAAACTCATCACTACA 2139
 SecI
 2099

2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTCTTCTCTCACC 2208
 Ksp632I
 METAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr
 2171

	SalI		HindII	NaeI	
			AccI	Cfr10I	
2209	AATGCCCTCCGTTGTGGAAAGTCGACGCAAGATGATGCCACAATCCAGCGGCCCATTT				2277
	AsnAlaSerValTyrArgThrValValGluValAlaAspGluAspAlaThrAsnProAlaGlyProPhe				
	2220		2241	2267	
			2242	2269	
			2240		

	Tth111II		
	HindIII	NlaIV	
2278	AGGATTCCAAAATGTAGGAAGGAGTTTCAGCAAGCACAAACACCTGAAAGCTTGCCAACACAATGGCTCCAC		2346
	ArgIleProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis		2342
			2325

	Tth111II	NlaIV	BbvII
2347	AAGCAGGCAATGCAGTCCGGTAGTGTCACAGCTGCACCCCTCGATGGTGAGTTTGATTTTGAAGACGAC		2415
	LysGlnAlaMETGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp		
	2363	2384	2415

	NlaIV	Apal	GsuI	HaeI	NspBII	SacI
						Ksp632
2416 GTGGAGAACCAACAGGCCCGCAGCAGAGGCCACCGCTGCTCCAGCAGTGCTGCAACGAGCTCCAC						
ValGluAsnGlnGlnGlyProGlnGlnArgProLeuLeuGlnGlnCysAsnGluLeuHis						
	2438	2444	2449	2455	2481	2484
	2436					

FIGURE 10

	AccI		
2830	TACTCCGTA	GACGGTAATAAAAGAGAAAGTTT	TTTACTCTTGCTACTTTCCCTATAAAGTGATGAT 2898
		2838	
		VspI	
			SpeI
			ScaI
2899	TAACAACAGATA	CACCAAAAAGAAAACAATTAAATCTATATTCAACAATGAAGCAGTACTAGTCTATTGAA 2967	
		2929	
			2954
			2955
	NspI		
	AflIII		
2968	CATGTCAGATTTTCTTTTCTAAATGTCTAATTAAAGCCTTCAAGGCTAGTGATGATAAAAGATCATCCA 3036		
	2968		
	XhoII		
	NlaIV		
	BamHI		
			MmeI
			BclI
3037	ATGGGATCCAACAAGACTCAAATCTGGTTTGTGATCAGATACTTCAAAACTATTTTGTATTTCATTAAA 3105		
	3041		
			3069
			3043

	BbvII		Tth111
3106	TTATGCAAGTGTCTCTTTTATTGGTGAAGACTCTTTTAGAAGCAAGAACGACAGCAGTAATAAAAAA		3174
	3139		
3175	ACAAAGTTCAGTTTAAAGATTGTGTTATTGACTTATTGTCAATTGAAAAAATATAGTATGATATTAATATA	VspI	3243
			3237
3244	GTTTATTATATAATAATGCTTGTCTATTCAAGATTTGAGAACATTAAATATGATACTGTCCACATATCCAA	VspI	3312
3250			3287
3313	TATATTAAGTTTCATTCTGTTCAAACATATGATAAGATGGTCAAAATGATTATGAGTTTGTATTAC	NdeI	3341
		Tth111II	3352
3382	CTGAAGAAAAGATAAGTGAGCTTTCGAGTTTCTGAAGGGTACGTGATCTTCATTCTTGGCTAAAAGCGA	Eco57I	3404
			3434
3451	ATATGACATCACCTAGAGAAAAGCCGATAATAGTAAACTCTGTTCTTGGTTTTTGGTTTAATCAAAACCGA	Eco57I	3519

Cfr10I
 |
 3520 ACCGGTAGCTGAGTGTCAAGTCAGCAAAACATCGCAAAACCATATGTCAATTTCGTTAGATTCCCGGTTTAA 3588
 3521
 Tth111II
 NdeI
 ||
 3560
 3561

 Cfr10I
 |
 3589 GTTGTAACCGGTATTTCATTTGGTGAAACCCCTAGAAGCCAGCCANCCTTTTAAATCTAATTTTGTGCA 3657
 3597

 NlaIV
 HindII
 HgiCI
 BspHI
 |||
 3658 AACGAGAAGTCACCAACCTCTCCACTAAACCCCTGAACCTTACTGAGAGAAGCAGAGNCANNAAGAA 3726
 3717
 3716
 3718

 Eco31I
 |
 3727 CAAATAAAACCCGAAGATGAGACCAACCGTGCGCGCGGACGTTTCAGGGGACGGGAGGAAGAGAAATGR 3795
 3740
 3756
 3781
 Ksp632I
 |
 3796 CGGCGG5MNTTTGGTGGCGGCGGACGTTTGGTGGCGCGGTGGACGTTTGTGGCGCGGTGGA 3864

FIGURE 10
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	EcoRV	
3865	CCTTTGGTGGATATCGTGACGAAGGACCTCCAGTGAAGTCATTGGTTCGTTACTCTTTTCTTAG	3933
	3880	
	HindIII	
	AflIII	
3934	TCGAATCTTATTCTTGCTCTGCTCGTTGTTTACCGATAAAGCTTAAGACTTTATTGATAAAGTTCTCA	4002
	3977	
	3974	
4003	GCTTTGAATGTGAATGAACGTGTTTCCTGCTTATTAGTGTTCCCTTTGTTTGAGTTGAATCACTGTCTTA	4071
4072	GCACTTTTGTAGATTCACTTTTGTGTTTAAAGTTAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG	4140
	HpaI	
	HindII	
4141	ACAAGTTAACTTTGTTGGTTATAACAGAAAGTTGCGACCTTTTCTCCATGCTTGTGAGGGTGATGCTGTG	4209
	4149	
	4179	
	XhoII	
4210	GACCAAGCTCTCTCAGGCGAAGATCCCTTACTTCAATGCCCCCAATCTACTTGGAAAACAAGACACAGAT	4278
	4231	